

SEQUENCE LISTING

<110> Kaneka Corp.
 OKUBO, Yuji
 MATSUMOTO, Keiji
 TAKAGI, Masamichi
 OHTA, Akinori

<120> NOVEL TRANSFORMANT AND PROCESS FOR PRODUCING POLYESTER USING THE SAME

<130> Q96497

<150> PCT/JP2005/003589
 <151> 2005-03-03

<150> JP 2004-061291
 <151> 2004-03-04

<150> JP 2004-062812
 <151> 2004-03-05

<160> 39

<170> PatentIn version 3.3

<210> 1
 <211> 102
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized restriction enzyme cleavage site

<400> 1
 aagctgcggc cgcagcttgc atgcctgcag gtcgactcta gaggatcctc gaggatcccc 60
 gggtagccta gcgtaccgag ctatccattt aaatccgaat tc 102

<210> 2
 <211> 1785
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized polynucleotide encoding mutant Aeromonas caviae phaC having mutation at codon 149

<400> 2
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ccagccagag tcccagaaga aggtttggct ccagctccag gtcactatgt caaagttaga 1740
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<210> 3
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically synthesized polynucleotide encoding *Ralstonia eutropha* phbB for expression in *Candida maltosa*

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<400> 3
atgactcaaa gaattgccta cgttactggg ggtatgggtg gtattgggtac tgctatattgt      60
caaagattgg ctaaagatgg ttttagagtt gttgctgggt gtgggtccaaa ctctccaaga      120
agagaaaaat ggttggaaca acaaaaagct ttgggttttcg attttattgc ttctgaaggt      180
aatgttgctg attgggattc tactaaaact gctttcgata aagtcaaadc cgaagtcggt      240
gaagttgatg ttttgattaa caatgctggg attactagag atgttggttt tagaaaaatg      300
actagagctg attgggatgc cgttattgat actaacttga cttctttgtt caatgtcact      360
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gttaatggtc aaaaagggtc atttggtcaa actaactatt ccactgctaa agctgggtttg      480
catggtttca ctatggcttt ggccaagaa gttgccacta aagggtgttac tgtcaatacc      540
gtctctccag gttacattgc tactgatatg gtcaaagcca ttagacaaga tgtttttagat      600
aaaattgtcg ccaccattcc agtcaaaaga ttgggttttcg cagaagaaat tgcttctatt      660
tgtgcttggt tgtcttctga agaatccggt ttttctactg gtgctgattt ctctttaaac      720
ggtggtttgc acatgggtta a                                     741

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<210> 4
<211> 754
<212> DNA
<213> Artificial Sequence

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<220>
<223> chemically-synthesized promoter with multiple alkane responsible
regions

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aagcttgcac gcctgcaggc cgaaattcga gctcgggtacc cggggatcct ctagagtcca      60
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ttttatccgc tcatgtgctt ttttttttgt tttcaatttg aaagtttttt tatttccgca      180
atacaaaatt attttttatc cgctgacca gatcctctag agtccatgtg cttttttttt      240
tgttttcaat ttgaaagttt ttttatttcc gcaatacaaa attatttttt atccgctcat      300
gtgctttttt ttttgttttc aatttgaaag tttttttatt tccgcaatac aaaattattt      360
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gttttcaatt tgaaagtttt tttatttccg caatacaaaa ttatttttta tccgctgacc      540
cagatctcga ctctagagga tccccgtttt tttatttccg caatacaaaa ttatttttta      600
tccgctttcc gttcctttct tcttgatgata aatctcaaca attatatata tcattccata      660

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<210> 5
 <211> 594
 <212> PRT
 <213> Aeromonas caviae

<400> 5

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Asn Asp Lys Leu Leu Ala Met Ala Lys Ala Gln Thr Glu Arg Thr Ala
 20 25 30

Gln Ala Leu Leu Gln Thr Asn Leu Asp Asp Leu Gly Gln Val Leu Glu
 35 40 45

Gln Gly Ser Gln Gln Pro Trp Gln Leu Ile Gln Ala Gln Met Asn Trp
 50 55 60

Trp Gln Asp Gln Leu Lys Leu Met Gln His Thr Leu Leu Lys Ser Ala
 65 70 75 80

Gly Gln Pro Ser Glu Pro Val Ile Thr Pro Glu Arg Ser Asp Arg Arg
 85 90 95

Phe Lys Ala Glu Ala Trp Ser Glu Gln Pro Ile Tyr Asp Tyr Leu Lys
 100 105 110

Gln Ser Tyr Leu Leu Thr Ala Arg His Leu Leu Ala Ser Val Asp Ala
 115 120 125

Leu Glu Gly Val Pro Gln Lys Ser Arg Glu Arg Leu Arg Phe Phe Thr
 130 135 140

Arg Gln Tyr Val Asn Ala Met Ala Pro Ser Asn Phe Leu Ala Thr Asn
 145 150 155 160

Pro Glu Leu Leu Lys Leu Thr Leu Glu Ser Asp Gly Gln Asn Leu Val
 165 170 175

Arg Gly Leu Ala Leu Leu Ala Glu Asp Leu Glu Arg Ser Ala Asp Gln
 180 185 190

Leu Asn Ile Arg Leu Thr Asp Glu Ser Ala Phe Glu Leu Gly Arg Asp
 195 200 205

Leu Ala Leu Thr Pro Gly Arg Val Val Gln Arg Thr Glu Leu Tyr Glu
 210 215 220

Leu Ile Gln Tyr Ser Pro Thr Thr Glu Thr Val Gly Lys Thr Pro Val
 225 230 235 240

Leu Ile Val Pro Pro Phe Ile Asn Lys Tyr Tyr Ile Met Asp Met Arg
 245 250 255

Pro Gln Asn Ser Leu Val Ala Trp Leu Val Ala Gln Gly Gln Thr Val
 260 265 270

Phe Met Ile Ser Trp Arg Asn Pro Gly Val Ala Gln Ala Gln Ile Asp
 275 280 285

Leu Asp Asp Tyr Val Val Asp Gly Val Ile Ala Ala Leu Asp Gly Val
 290 295 300

Glu Ala Ala Thr Gly Glu Arg Glu Val His Gly Ile Gly Tyr Cys Ile
 305 310 315 320

Gly Gly Thr Ala Leu Ser Leu Ala Met Gly Trp Leu Ala Ala Arg Arg
 325 330 335

Gln Lys Gln Arg Val Arg Thr Ala Thr Leu Phe Thr Thr Leu Leu Asp
 340 345 350

Phe Ser Gln Pro Gly Glu Leu Gly Ile Phe Ile His Glu Pro Ile Ile
 355 360 365

Ala Ala Leu Glu Ala Gln Asn Glu Ala Lys Gly Ile Met Asp Gly Arg
 370 375 380

Gln Leu Ala Val Ser Phe Ser Leu Leu Arg Glu Asn Ser Leu Tyr Trp
 385 390 395 400

Asn Tyr Tyr Ile Asp Ser Tyr Leu Lys Gly Gln Ser Pro Val Ala Phe
 405 410 415

Asp Leu Leu His Trp Asn Ser Asp Ser Thr Asn Val Ala Gly Lys Thr
 420 425 430

His Asn Ser Leu Leu Arg Arg Leu Tyr Leu Glu Asn Gln Leu Val Lys
 435 440 445

Gly Glu Leu Lys Ile Arg Asn Thr Arg Ile Asp Leu Gly Lys Val Lys
 450 455 460

Thr Pro Val Leu Leu Val Ser Ala Val Asp Asp His Ile Ala Leu Trp
 465 470 475 480

Gln Gly Thr Trp Gln Gly Met Lys Leu Phe Gly Gly Glu Gln Arg Phe
 485 490 495

Leu Leu Ala Glu Ser Gly His Ile Ala Gly Ile Ile Asn Pro Pro Ala
 500 505 510

Ala Asn Lys Tyr Gly Phe Trp His Asn Gly Ala Glu Ala Glu Ser Pro
 515 520 525

Glu Ser Trp Leu Ala Gly Ala Thr His Gln Gly Gly Ser Trp Trp Pro
 530 535 540

Glu Met Met Gly Phe Ile Gln Asn Arg Asp Glu Gly Ser Glu Pro Val
 545 550 555 560

Pro Ala Arg Val Pro Glu Glu Gly Leu Ala Pro Ala Pro Gly His Tyr
 565 570 575

Val Lys Val Arg Leu Asn Pro Val Phe Ala Cys Pro Thr Glu Glu Asp
 580 585 590

Ala Ala

<210> 6
 <211> 246
 <212> PRT
 <213> Ralstonia eutropha

<400> 6

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 20 25 30

Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln

35					40					45					
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Glu	Val	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Val	Val
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Phe	Arg	Lys	Met	Thr	Arg	Ala	Asp	Trp	Asp	Ala	Val	Ile	Asp	Thr	Asn
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<223> chemically-synthesized ADE1 gene

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caaaaaaata aaggctgtga gtttcgagcc aataattatg aattagtggg atttttttta	180
aagataaata atcaagaatc gcattaggga gacgaatatg cgttattcaa ataaaaagac	240
aattctttta gggtagcatt tcccttcaag ttcacccac atgtacatta atgtcaatga	300
tgtcgcagaa gttaaattag cagaagaaaa aaaaatgtg aattactccg agtcaactct	360
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gctcccagat gacttcaact aacttagaag gaactttccc attgattgcc aaaggtaaag	480
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ccgcatacga tgtgattatg tctaattgga tcccaaataa aggtaaaatc ttaaccaa	600
tgtctgaatt ctggtttgat ttcttgccaa ttgaaaacca ttaatacaaa ggagacattt	660
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cgagtaacag tatgattttt ttccctctcc cgtcgattga ggtttttttt ttctctttcg	1620
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<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

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<220>
<223> chemically-synthesized PCR primer

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<400> 8
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<210> 9
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<212> DNA
<213> Artificial Sequence

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<220>
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<400> 9
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<210> 10
<211> 35
<212> DNA
<213> Artificial Sequence

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<220>
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 <210> 12
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 <210> 13
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 <212> DNA
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 <400> 13
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 <210> 14
 <211> 34
 <212> DNA
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 <400> 14
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 <210> 15
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 <400> 16
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<210> 17
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 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 18
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<210> 19
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<210> 20
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 <212> DNA
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<220>
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 <400> 21
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<210> 22
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 <212> DNA
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 <400> 22
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<210> 23
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<220>
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 <400> 23
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<210> 24
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 <212> DNA
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 <400> 24
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<210> 25
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 <212> DNA
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<220>
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 aacaaaccaa atgatcttgt cgtg 24

<210> 26
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 <220>
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 <210> 28
 <211> 83
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized linker

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 tttaactcac atatgaagat atc 83

 <210> 29
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 <212> DNA
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 <210> 30
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 <212> DNA
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 <220>
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 <210> 31

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 <220>
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 <400> 31
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 <210> 36

<211> 31
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 <220>
 <223> chemically-synthesized PCR primer

 <400> 36
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<210> 37
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized PCR primer

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<210> 38
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 <400> 38
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<210> 39
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 <400> 39
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